

Ex 12  
 5' AGA GGG AATTCGGCAGCAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC  
 3' GAA GAA CAG 24  
 NT p16.207 1  
 Ex 1  
 ACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTG  
 Ex 13  
 NT p16.3  
 GAGGCGGTGGCGCTGCCCAACGCACCGAATAGTTACGGTCCGAG  
 I(2) I(1)  
 Ex 14  
 GCCGATCCAGGTCATGGATGATGGGCAGCGCCCCGAGTGGCGGAG  
 Ex 2  
 Exon 2  
 CTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCA  
 p16 INT  
 CTCTACCCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCTGGAC  
 NT p16.5  
 ACGCTGGTGGTGTCTGCACCGGGCCGGGCGCGGCTGGACGTGCGC  
 Ex 3  
 GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGC  
 CATCGCGATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGGCACC  
 15  
 AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTC  
 I(2) Ex 8 Ex 4  
 ACACATCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTC  
 Ex 5  
 GGGAAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCCACA  
 ACTGCCCCCGCCACAACCCACCCCGCTTTCGTAGTTTTTCATTTAGA  
 AAATAGAGCTTTTAAAAATGTCCTGCCTTTTAAACGTAGATATAA  
 GCCTTCCCCCACTACCGTAAATGTCCATTATATCATTTTTTATAT

Figure 1A

BBDET0-6989T060

ATTCTTATAAAAATGTAAAAAAGAAAAACACCGCTTCTGCCTTT

TCAGTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCG

CACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCTCCGGAAG

CTGTGACITCATGACAAGCATTTGTGAACTAGGGAAGCTCAG

GGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGCAG

AACCAAAGCTCAAATAAAAAATAAAATTATTTTCATTCATTCACT

CAAAAAAA

Figure 1B

Figure 2A

p16EX1 < GGNGGNAAGNTGTGGGGGAAAGTTTGGGGATGGAANACCAANCCCTCCTTTTCNTTACCAA 60  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCCGGGGGAGACCCAACCTGGGNC 120  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCANx 180  
p16EX13 < TCNCTTATTGNTAGGANATAATAACACCTCCACCGATAACT 41  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCGxGxTCCCTCCAGAGGATTTGAGG 240  
p16EX13 < TcaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCCTCCAGAGGATTTGTGG 101  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < GACAGGNTCGGAGGGGGCTCTTCCCCCANCACCGGAGGAAGAAAGAGGAGGGNCTGACTG 300  
p16EX13 < GACAGGGTNGGAGNGGTCTCTTCNCCACCACCGGAGGAAGAAAGAGGAGGGGCTGNCTG 161  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < GTCACCAGAGGGTGGGACGGACCGCTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA 360  
p16EX13 < TTCACCAGAGGGTGGGACGGACCNCGTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT 221  
.....+.....+.....+.....+.....+.....+.....+  
p16EX1 < CAACGGGCGGCGGGGAGCAGCATGGATCCGGCGGGCGGGGAGCAGCATGGANCCTTCGACT 420  
p16EX13 < CANCGGNCGNCGGGGAGCAACATGGAACCGNCGGCGGGGAGCAGCATGGANCCTTCGGCT 281  
.....+.....+.....+.....+.....+.....+.....+  
P16NT2 ? < GACNNNCTCCGGCCGNGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG 49  
p16EX1 < GACTGACTGCCTCGC 435  
p16EX13 < GACTGGCTGNCCACGNCCACGNCCCGGGTTCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG 341  
.....+.....+.....+.....+.....+.....+.....+  
P16NT3 > < E+13 > GTGTNANCCCGGTA 15  
P16NT2 < GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCAGGTxxGGGTA 109  
p16EX13 < GCGGGGNCTCTGNCCAACNCGCTAAAN 369  
.....+.....+.....+.....+.....+.....+.....+  
P16NT3 > GAGGGTCTGCAGCGGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG 75  
P16NT2 < GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG 169  
.....+.....+.....+.....+.....+.....+.....+  
P16NT3 > AATTGGAATCAGGTAGCGCTTCGANTCTCCGAAAAAGGGGAGGCTTCCTGGGGAGTTNN 135  
P16NT2 < AATTGGAATCAGGTAGCGCTTCGATTCTCNGAAAAAGGGGAGGCTTCCTGGGGAGTTT 229

# Figure 2B

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.....+.+.+.+.+.+.+.+.+.+.
> CAGAAGGGGTTTGTAAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGTTGGGAAGCCA 195
< CAGAAGGGGTTTGTAAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGGCTTGGGAAGCCA 289

.....+.+.+.+.+.+.+.+.+.+.
> AGGAAGAGGAATGAGGAGNCACGCGCNTACAGNTCTCTCGAATNCTGANAAGATCTGAAG 255
< AGGAAGAGGAATNAGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTNAAG 349

.....+.+.+.+.+.+.+.+.+.+.
> GGGGGAACATATTTGTATTAGxATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAA 315
< GGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANTxC      404

.....+.+.+.+.+.+.+.+.+.+.
> CGTGTGGNATAAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC 375

.....+.+.+.+.+.+.+.+.+.+.
> CAANACACAGATNCCTGGATGGAGCT                                     401

.....+.+.+.+.+.+.+.+.+.+.

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09016869.013098

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6INT      > AAAANNAAAAAAAAAATCTCCCAGGCCTAACATAATTNTCAGGAAAGAAATTTTCAGTAGTTG 60
          .....+......+......+......+......+......+
6INT      > NATCTCAGGGGAAATACAGGAAGTTAGCCTGGAGTAAAAGTCAGTCTGTCCCTGCCCCTT 120
          .....+......+......+......+......+......+
6INT      > TGCTANATTGCCCGTGCCCTCACAGTGCTCTCTGCCTGTGACGACAGCTCCNCAGAAGTTC 180
          .....+......+......+......+......+......+
6INT      > GGAGGATATAATGGAATTCATTGTGTACTGAAGAATGGATAGAGAACTCAAGAAGGAAAT 240
          .....+......+......+......+......+......+
6INT      > TGGAAACTGGAAGCAAATGTAGGGGTAATTAGACACCTGGGGCTTGTGTGGGGGTCTGCT 300
6EX15    < AANAAAAaAgAAATNgAtAANATagAGGAaT 31
          .....+......+......+......+......+......+
6INT      > TGGCGGTGAGGGGGCTCTACACAAGCTTCCTTTCCGTCATGCCGNCCCCACCCTGGCTC 360
6EX15    < GATCANATTAATAATCAAAAAAGANAAGANAGAcTaATAAAAAACGAgATgTTeTAGAS 91
          .....+......+......+......+......+......+
6INT      > TGACCATTTCTGTTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTG 420
6EX15    < NTAATcATAATTATAaaaggTeAagacTcATTGATATnaAGGAaattgaAGGGAATetTa 151
          .....+......+......+......+......+......+
6INT      > CTGCTGCTCCACGGCGCGGAGCCCAACTGCTCCGACGCCG 460
6EX15    > CCTGCNACGACCCCGCCACTCTCACCCGACCCGTG 35
6EX14    > NCTCTCACGGTGGGGAGGCCAACTGCGCCGAACCCGCCACTCTCACCCGACCCGCG 56
6EX15    < acTagCACANNNGNATNAANAANAATTccacGACACCGCCACTCTCAACCGATCCGTG 211
          .....+......+......+......+......+......+
6EX2     > CACGACGCTGTCCGGGAGGGTTTCTGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGNG 95
6EX14    > CACGACGGTGCCCGGGAGGGGTTTCTGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGCG 116
6EX15    < CTCGACACTGCCCGGGAGGTCNTCTGGACACGCTGGTGGTNCTCCACCGGNCCGGGGCA 271
          .....+......+......+......+......+......+
6EX2     > CGGTTGGACGTGCGCGATGCCTGGGGCCGCTNCCCGTGGxACCTGGTTGAGGAGCTGGG 155
6EX14    > CGGCTGGACGTTTCGNGATGCCTGGGGGCNTCTNTCCGTNGxACCTGGCTGAAGAGCTGGN 176
6EX15    < CGTCTGGACGTGCGCGATGCCTGGGNCCGNCTACCCGTGGTACCTGACTGAGGACCTGGG 331
          .....+......+......+......+......+......+
6EX2     > NCATCGCGATGTGCGACGGSTACCTGCGCGCGGTTGCGGGGGGGCACCAGAGGxNAGTNACC 215
6EX14    > NCATCGNGATGTGCGACGGCCNCTGTGTGNGGNTGCGGGGGGGCACCATAGGTCAGTNTCC 236
6EX15    < CCATCCCGATTTCGCGNGGGTANCTGNGNGNGGGCTGNGGGGGGCCAANAGAGGxCANTACCC 391

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0  
▷16EX  
▷16EX  
1  
0  
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▷16EX  
▷16EX  
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=

0  
▷16EX  
▷16EX  
0  
0  
▷16EX  
▷16EX

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>16EX4          > AGAAATTAGATCATCAGTCACCGATG 26
>16EX5          < TTGAAAGAACCAGAGAGGGCTCTGAGAAACC 570
>16EX9          < TTGAAAGAACCAGAGAGGGCTCTGAGAAACCTCCGGAACCTTAGxTCATCAxTCGCCGNAA 424
               .....+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+
>16EX4          > GTCCTACAGGGNCACAACCTGNCCCCGCCACAACCCACCCCGNTTTCGTAGTTTTCATTTA 86
>16EX9          < AA 426

```

6-EX  
6-EX  
6-EX  
6-EX

# Figure 3C

16EX6a > GNGGATTGGNCCACTACGCNTANCCATCACCCCTATTC 515

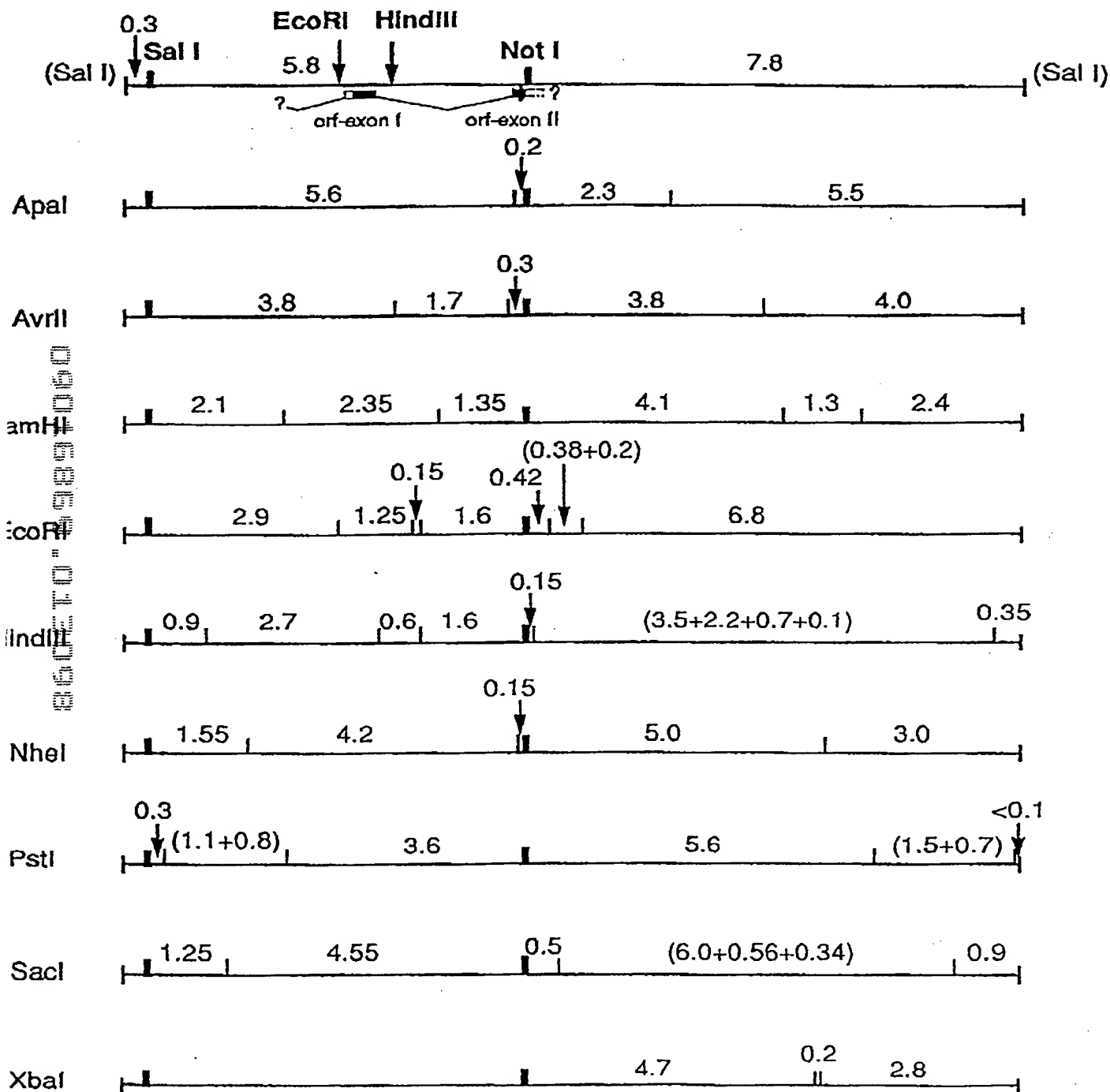
.....+.....+.....+.....+.....+.....+

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Figure 5



[illegible]